

Reinheit number	Gram-negative Bacteria
Staphylococcus	
Escherichia coli (115)	L LTPSO T FVF ...
Proteus mirabilis (115)	L LTPK H FVF ...
Haemophilus influenzae (136)	L LTPIO K KVF ...
Pseudomonas putida (133)	K LTPRH KAVP ...
Buchnera apicis (114)	K LKSTPH KAVP ...
Salmonella typhi (115)	L LTPAH T PVP ...
Yersinia pestis (139)	L LTPSH T PVP ...
Klebsiella pneumoniae* (119)	L LTPSH T PVP ...
Salmonella paratyphi (119)	I PATST I PVP ...
Vibrio cholerae (123)	I PATSO K PVP ...
Pseudomonas aeruginosa (135)	K LTAPO SAVP ...
Shewanella putrefaciens# (118)	L LTPAO K SVF ...
Alphaproteobacteria	
corynebacterium (121)	M MTTAE ARRY ...
Caulobacter crescentus (139)	T S S KHOKE RLLA ...
sp. Rhizobium	E E RKKRPD LLLA ...
Helicobacter pylori 16655 (161)	D S KKKSE DRVY ...
Helicobacter pylori 395 (161)	D S KKKSE DRVY ...
Campylobacter jejuni* (108)	D STNNE SSVY ...
Beta-Deltabac.	
Neisseria gonorrhoeae* (122)	T LKTTDD SSUV ...
Neisseria meningitidis* (123)	A LKTTDD SSVF ...
Bordetella pertussis* (123)	A CHAPSE AAAL ...
Thiobacillus ferrooxidans (116)	D BROKVA FORTL ...

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Genus	Species	Antibiotic	Sensitivity	Resistance
Bacillus	<i>Bacillus subtilis</i> (123)	H	R R R E D	L V C D R I L S A
	<i>Streptomyces coelicolor</i> (123)	H	R R R E D	L V C D R I L S A
	<i>Micobacterium luteum</i> (123)	R	R T P A E	L V Q R A V A Q M R
	<i>Mycobacterium tuberculosis</i> (125)	R	R T P A E	L V Q R A V A Q M R
	<i>Mycobacterium leprae</i> (120)	N	R R R S S E	L V A R T N L O E
	<i>Mycobacterium bovis</i> (115)	N	R R R S S E	L V A R T N L O E
	<i>Mycobacterium avium</i> * (119)	N	R R R S S E	L V A R T N L O E
	<i>Corynebacterium diphtheriae</i> * (129)	H	R S Q R A T I	L V A R T N L O E
Lau G.C.	<i>Kine</i>	H		L V A R T N L O E
	<i>Bacillus subtilis</i> (119)	H	K R S D D	O K V F
	<i>Bacillus halodurans</i> (118)	H	K K K D E	S R V P
	<i>Bacillus anthracis</i> (119)	H	K K K D E	S R V P
	<i>Mycoplasma capricolum</i> (1021)	H	K K K F E	S R V P
	<i>Mycoplasma pneumoniae</i> (118)	H	R V D R K E	S R V P
	<i>Mycoplasma genitalium</i> (128)	H	R R K V	A A I L
	<i>Streptococcus pyogenes</i> (113)	H	S R R K Y	V V I S
	<i>Streptococcus suis</i> (119)	H	R S D E D	V V I S
	<i>Streptococcus pneumoniae</i> (124)	H	K R E D D	V V I S
	<i>Staphylococcus aureus NOC*</i> (117)	Y	P F K N A D	V V I S
	<i>Staphylococcus aureus CO*</i> (117)	Y	P F K N A D	V V I S
	<i>Staphylococcus difficile</i> * (114)	K G	K K N S D	R K V

Thermococcus *martini* (117) ... G ■■■■■ R L R D E L L I F V ... ■■■■■ L R I V K R E ■■■■■ P G K D T R M N S K L ■■■■■ W V ■■■■■ Z I P R R N K G V ■■■■■ ■■■■■ V I P R N K L S E E P E R V U D P M T E R E K - - - - - L
 Bacteroides *populeum* (137) ... G ■■■■■ Y L R D E S E N T V P ... S ■■■■■ H E V S A M E R P R R E K ■■■■■ R V A M E L ■■■■■ P A Y R L N K H L ■■■■■ ■■■■■ L Q E R O Q I Y A T T A P H V V S D E ■■■■■ P D P T V E R A ■■■■■
 Deltopsocii
 Deinococcus *radiodurans* (166) ... ■■■■■ R G E R E E R K V R ... ■■■■■ I L V U S S H S T L K H E K ■■■■■ R A E R V E Z A L R T H P P E - W ... R ■■■■■ L N L N P G V U L T V P V P E L Q A ■■■■■ A Q A L Q R G E G ...
 Green-Shulfur
 Chlorobium *tephrae* (129) ... A ■■■■■ X G G - ■■■■■ L L I ... ■■■■■ V ■■■■■ F T G ■■■■■ L V P R D ■■■■■ D E R I T L H E C A Y R L E K H I - ■■■■■ H O N - ■■■■■ N A P L Y H A R A D A I P S - ■■■■■ E R P R A I R H E M ...

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Streptococcus mutans UAB159 (119 aa)

Amino acid sequence:

VLKKAYRVKSDKDFQAI FTEGRSVANRKFVVYSLKDQSHYRVLGVLSVGKRLGNNAVRNAIKRKLHVLMELGPYLGT
QDFVVIARKGVEELDYSTMKKNLVHVLKAKLYQEGSIREKE

Nucleotide sequence (plus strand):

AGATTTGGCTTCTCATTTATGATAATTAAATATTGGAGTCAT **GTTTGAAAAAGCTA**
TCGCCTTAAAGTATAAAGATTTCAGGCAATTTCAGTGAAGGACGAAGTGTGCCAATCGGAAATTGTTGCT
ATAGTTAGAAAAGATCAAAGTCACTATCGTGTGGACTTCAGTGGAAAAGATTAGGAAATGCTGTCGTTAGA
AATGCGATTAACGAAAATTGCGCCATGCTCTATGGAACTTGGCTTATTTAGGCACTCAAGATTGTTGTTAT
TGCTAGAAAAGGTGTTGAGGAATTGATTATAGCACGATGAAAAAAACTGGTCATGTTAAAACGGCTAAC
TGTATCAGGAAGGATCTTCGTAAAAAGAA

Sequence origin: University of Oklahoma ACGT; Contig 299

FIG. 2A

Klebsiella pneumoniae M6H 78578 (119 aa)

Amino acid sequence:

VVKLAFPRELRLTPSHFTFVQQPQRAGTPQITILGRLNSLGHPRIGLTVAKKNVRAHERNRIKRLTRESFRLRQ
HELPPMDFVVVAKRGVADLDNRALSEALEKLWRRHCRLARGS

Nucleotide sequence (plus strand):

CGTCGTCGTCTAAAGGCCGCGCTCGTCTGACCCTTCCAAGTAATAAAGCTAACCCCTGC **GTGGTTAAGCTCGCATT**
TCCCAGGGAGTTACGCTTGTAACTCCCAGTCATTCACTTCTGCTTCCAGCAGCCACAACGGGCTGGCACGCCGC
AAATCACCATCCTCGCCGCTGAATTGCTGGGGCATCCCCGATCGGTCTCACCGTCGCCAAGAAAAACGTGAAA
CGCGCACATGAACGCAATCGGATTAAACGTCGACGCGTGAAGTTTCGTTGCGTCAACATGAACTCCGCCAAT
GGATTCGTTGGTGGTGGCGAAAAGAGGGGTTGCCGACCTCGATAACCGTGCTCTCGGAAGCGTTGGAAAATTAT
GGGCCGCCATTGTCGCCTGGCTCGCGGGTCT **TGAT** CGGCCTGATTGAGTTATCAGGCCCTGATTAGTCCGCTAC
TCGGGCCGCATTGTC

Sequence origin: Washington University; Contig 632

FIG. 2B

Salmonella paratyphi A ATCC 9150 (110 aa)

Amino acid sequence:

VTFVNSRSFHRLPATSTGCTPQITILGRLNSLGHPRIGLTVAKNVRAHERNRIKRLTRESFRLRQHELPAMDFV
VVAKKGVADLDNRALSEALEKLWRRHCRLARGS

Nucleotide sequence (plus strand):

CTGACCGTTCCAAGTAATAAAGCTAACCCCTGAGTGGTTAACGCTGCATTCCAGGGAG**TTAC** GTTTGTTAACTC
CCGCTCATTTCACATTGCTTCCAGCAACCTCAACGGGCTGCACGCCGCAAATCACCATTCTGCCGCTGAATT
CGCTGGGGCATCCCCGTATCGGTCTTACCGTCGCCAAGAAAATGTTGACGTGCGCATGAACGCAACCGGATTAAA
CGTCTGACGCGTGAAAGCTTCCGCTGCGCCAGCATGAACCTCTGCAATGGATTCTGTTGGTGGCGAAAAAAAGG
GGTTGCCGACCTCGATAACCGTGCTCTCGGAAGCGTTGGAAAAATTATGGCGCCGCACTGTCGCTGGCTCGCG
GGTCCTGATAG CCCTTATTGCGGTCTATCAACGCCCTGATCAGTCCGCTGCTGGCCGCATTGTCGTTTC

Sequence origin: Washington University;

FIG. 2C

Pseudomonas aeruginosa PAO1 (135 aa)

Amino acid sequence:

VVS RDF DRD KRL LTA RQF SAV FDS P T G K V P G K H V L L A R E N G L D H P R L G L V I G K K N V K L A V Q R N R L K R L I R E S F R H N
Q E T L A G W D I V V I A R K G L G E L E N P E L H Q Q F G K L W K R L L R N R P R T E S P A D A P G V A D G T H A

Nucleotide sequence (plus strand):

T C T G T C G C G T C G T C G C C A A A G G C G T A A G C G T C T G A C C G T C T G A T T T A T C C G G T A C C G G G G G A C T T
C G A C C G G G A C A A G C G T C T A C T G A C A G C C C G G C A A T T C A G C G C A G T C T T C G A C T C T C G A C C G G C A A G G T C C C C G G C A
A G C A C G T C C T G C T G C T G G C G C G G A A C C G G T C T C G A T C A C C C C C G C T G G G C T G G T G A T C G G C A A G A A C G T C
A A G C T C G C C G T C C A G C G C A A T C G C C T C A A A C G C C T G A T C C G C G A A T C G T C C G C C A T A A C C A G G A A A C C C T G G C T G G
C T G G G A T A T C G T G G T G A T C G C G C G A A A G G C C T G G G C G A C T G G A A A A T C C G G A G C T G C A C C A G C A G T T C G G C A A G C
T C T G G A A A C G C C T G T G C G C A A T C G A C C T C G C A C G G A A A G G C C T G C T G A C G C C C C T G G C G T G G C C G A C G G T A C T C A T
G C A T A G G T C G A T G C C C G C G C A T C C C G A T C C C T G T A G T G T C A T C C C C C C T G A T G A C C C G G C A C C G

Sequence origin: Pathogenesis & University of Washington; Contig 54

FIG. 2D

Corynebacterium diphtheriae (129 aa)

Amino acid sequence:

V T L T S S N R T T V L P S Q H K L S N S E Q F R A T I R K G K R A G R S T V V L H F Y A E A T A G N L A T A G G P R F G L V V S K A V G N A V T R H R V
S R Q L R H V V I A M K D Q F P A S S H V V V R A I P P A A T A S Y E E L R A D V Q A A L D K L N R K R

Nucleotide sequence (plus strand):

C C G G T C G C G C A A T C G T G G C T G C A C G T C G T A A C A A G G G T C G T A A G A G G C C T G A C C G C T T A A G G T C A C T C T T A C A A G C T C
G A A T A G A A C G A C G G T G C T A C C T C A C A G C A C A A G G T C A G C A A T T C C G A A C A G T T C C G C G C A A C G A T T C G G A A G G G C A
A G C G T G C T G G G A G G A G C A C C G T C G T C T C A T T T T A T G C T G A G G G C G A C C G C G G G C A A C C T T G C A A C C G C A G G G C G G C
C C G C G A T T C G G C C T C G T G T G C T C A A G G C T G T G G A A A T G C T G T G A C T C G T C A C C G T G T T C G C G G C A G T T A A G G C A
C G T A G T A A T C G C T A T G A A A G A C C A G T T C C C A G C G T C A T C C C A T G T G T G A G G G G C A T A C C G C C A G C G G C G A C A G
C C A G T T A T G A G G A G T T G C G G G C A G A T G T G C A G G C A G C A C T C G A C A A G G C T C A A C C G C A A G C G A T A A G G C G G T T A C T C G
C C C T C G T G G G C T G G T T A G T C G C G C A T T G T T G A T G C G G T G C G G T T C T A

Sequence origin: Sanger centre; Contig 390

FIG. 2E

Chlamydia trachomatis MoPn (119 aa)

Amino acid sequence:

V H R L T L P K S A R L L K R K Q F V Y V Q R C G Q Y C R T D Q A T L R I V P S R H S N I R K V G V T V S K K F G K A H Q R N R F K R I V R E A F R H V R
P N L P A C Q V V V S P K G G T L P N F G K L S A D L L K H I P E A L P L V T S S K

Nucleotide sequence (plus strand):

G C T A C A A A A A G T G G A A G A A A T C T T T A A T C G T C G C C G T C A C G G C A G A C A T T C C T T A A T T G A T C T C A A G A T C T
T T C A T T T G T G C A T C G G T T A A C T C T A C C T A A A A G T G C C C G C T A T T G A A A C G T A A A C A A T T G T T A C G T G C A G C G T T
G T G G G C A A T T G T C G T A C T G A T C A G G C A A C T T A C G A A T A G T T C C T C G T C A T T C G A A C A T C C G T A A A G T A G G G
G T T A C T G T T C T A A A A A T T G G G A A A G G C C A T C A G C G C A A T C G C T T A A A G A A T T G T G C G A G A G G C T T T A G G C A
T G T G C G A C C A A A T C T T C C C G C A T G T C A A G T G G T A G T G T C T C C T A A A G G G G C A C T C A C C A A A T T T G G T A A A C T A T
C C G C G G A T C T T C T T A A G C A T A T T C C A G A G G C T T T G C C T C T C G T T A C T T C T C A A G T A G T T T T A T T T G G T C A A A
A A A T A A A A A A C C A T C C A C G C T A T A G A G G C A T G G A T G G G A A T G G G A A

Sequence origin: TIGR & Manitoba University;

FIG. 2F

Streptococcus pyogenes M1 (113 aa)

Amino acid sequence:

VKREKDFQAI FKDGKSTANRKFVIYHLNRGQDHFRVGISVGKKIGNAVTRNAVKRKIRHVIMALGHQLKSEDFVIA
RKGVESLEYQELQQNLHHVLKLAQLEKGFSEEEKH

Nucleotide sequence (minus strand):

GTTACCTCACCAACGACCACAGGCCACTAATAATAGAACTAAGGGACTATTCTGCAATT **TTAATGTTTCTTCAC**
TCTCAAAACCTTCTCAAGCAATTGTGCTAACCTTAAACATGATGTAATTGTTGAAGCTCTTGATACCTCAA
GATTGACACCCCTACGGCAATCACCACGAAATCCTCTGACTTCAGCTGATGCCCTAATGCCATGATAACATGACG
TATCTTCGTTGACTGCATTCTGGTACTGCATTCTATTGTTACCGACAGAAATACCCACACGGAAGTGGT
CTTGGCCTCTATTAAATGATAAAATTGACAAATTTCGATTGCTGACTTTCCATCCTTAAATATGGCTTGAAA
TCTTCTCACGCTT **GACACGATAGGTCTTCTCAAAATTAACTCCAATATCTAAATTATTACCATACACATC**

Sequence origin: University of Oklahoma ACGT; Contig 7

FIG. 2J

Bordetella pertussis Tohama I (123 aa)

Amino acid sequence:

MPRATLPAEARLHRPSEFAAALKGRRRLARGAFFIVSASPCAPADDQPARARLGLVIAKRFAARAVTRNTLKRVIREA
FRARRRLALPAQDYVVRLLHSKLTPASLTALKRSARAEVDAHFTRIAR

Nucleotide sequence (minus strand):

CCACCCAGGGCTGAGGAAGTACCGTAAACCGGATGGGGCGATAAGCAGTCTCCTGAT**CATCGCGCTATCCGTG**
TGAAGTGAGCATCTACTCGGCGCGCCGAGCGTTCAAGGGCCGTGAGGCTTGCCGGTGTAGCTTGCTGTGCAGC
CGCACACGTAATCCTGGGCCGGCAGGGCAAGCCGGCAGGCCGAACGCTTCGCGGATGACCCGTTCAAGGTATT
GCGCGTCACGGCGGGCGGAAAACGCTTGGCGATCACCAGGCCAGGGCGCGCGCGCCGGCTGGTCATCAGCAG
GGGCACAGGGCGAGGCCTGACAATAAAAGAAAGCCCCTGGGCCAGTCGCCGGCTTGAGGGCGGGCAAACCTCG
GAGGGCGATGCAATCGGCCCTCCGCAAGGGAGCGTGGCGCGGG**CATGGGTGACGTGACGGAGACTGGCGACGGGGC**
CGCGCGGATGCTCCTGTTACAGGCAATCC

Sequence origin: Sanger centre & MDS; Contig 267

FIG. 2K

Porphyromonas gingivalis W83 (137 aa)

Amino acid sequence:

MTSPPTFGLSKSERLYLRDEINTVFGEKGAFVVYPLRVVYRLGSEHRVAYSSMLVSVAKKFRRAVKRNRVKRLVRE
AYRLNKHLLNDVLQERQIYATIAFMVSDELPDFRTVERAMQKSLIRIAGNPSSALKNE

Nucleotide sequence (minus strand):

AGAAGAAAATGGGGAGCAGTAAGAGTGCACGAGAAAAGCCTTGATCAGTCGCATCGTATT **TACTCGTTTCAAAG**
CCGATGAAGGTACATTCCGGCAATTCTGATCAGACTCTTGCATCGCTCTCCACTGTCAGAAAGTCAGGAAGT
TCATCCGATACTACCATAAATGCAATAGTAGCATAGATCTGCTCTGGAGGACATCGTCAGGAGGTGTTGTT
GAGCCGATAAGCCTCCCTGACCAACGCTTGACCCATTGGCGCTCACGGCTCGCCTAAACCTTTCTTGCTACGC
TTACCAGCATGGAGGAATATGCAACTCGATGCTCCGATCCAGACGGTAGACTACCGTAGAGGATAAACGACA
GCCTTGCCCTGCCAAAGACCGTATTGATTTCATCGCGAAGATAGAGGCCTCGCTTGGATAGGCCAATGTAGG
CGGAGAGGT**CATTCCCGTTGAGGTAATCCTCTAATGCCATAGCCATAGAAGGATATTGCTCGGTGGCGCA**

Sequence origin: TIGR & Forsyth Dental Center

FIG. 2L

Streptococcus pneumoniae Type 4 (124 aa)

Amino acid sequence:

VLKKNFRVKREKDFKAI FKEGTSFANRKFVYQLENQKNRFRVGLSVSKLGNAVTRNQIKRRIRHIIQNAKGSLVE
DVDFVVIARKGVETLGYAEMEKNLHVLKLSKIYREGNGSEKETKVD

Nucleotide sequence (minus strand):

TCGCTAGTTACCCCATTAGTCGCACAGGCTGTCATGATTAACAGAGACAGTCCTAGCAAACTAGTCAACTTTAGTT
CTTTTCACTCCCATTTCTCCGGTAAATCTTGATAATTAAATACATGGAGTAGATTTCTCCATCTGCG
TATCCAAGGTTGACTCCTTTGAGCAATGACAACAAAGTCGACATCTTCTACCAGACTCCCTTGCATTCTG
GATAATATGCCGAATCCGTCGCTTAATTGATTCTAGTGACGGATTCCCCAGTTTGCTAACTGATAGACCTA
CTCGAAAACGGTTTCTGGTTCTAATTGGTAGACCACAAATTGCGATTAGCAAACTGTCCCCTCCTGAAA
ATCGCCTAAATCTTCTCTTTACACGAAAGTTCTTCAAAACTCAACTCCATCTATTAAATTACTACTA
TTATACCATTTTCAAAAAAGCCAATCATAG

Sequence origin: TIGR;

FIG. 2M

Clostridium difficile 630 (epidemic type X) (114 aa)

Amino acid sequence:

MDFNRTKGLKKDSDFRKVYKHGKS FANKYLVIYILKNKSDYSRVGISVSKVGKAITRNVRRLIKEAYRLNIDEKI
KPGYDIVFIARVSSKDATFKDIDKSIKNLVKRTDISI

Nucleotide sequence (minus strand):

TCCTTAATATAAATTATTTATTCAAAGTCATTAACCTCCATATTATAGCATACAATTAAATAGAAATATCCG
TTCTTTAACTAAATTTTATAGACTTGTCTATGTCTTAAAGTAGCATCCTACTAGATACCCTTGCTATAAAAT
ACTATATCATATCCAGGCTTAATTTCATCAATATTAAACTGTAGGCTTCTTTATTAATCTCTTACTCTATT
CCTAGTAATAGCTTCCACTTTTTGAAACAGAATACCTACTCTACTATAATCTGATTATTTAAAGTATAT
ATATTACTAAATATTGTTGCAAAGATTGCCGTGTTATATACTTTCTAAATCAGAGTCTTTCAACCC
TTAGCCTATTAAAGTCCATAGTTAACCTCCATAAACACAGCTATGAATCGTAATTATTCACACAAAAGGCCACCT
TTG

Sequence origin: Sanger centre; Contig 975

FIG. 2N

Camphylobacter jejuni NCTC (108 aa)

Amino acid sequence:

VKNFDKFSTNEEFSSVYKVGKKWHCEGVIIFYLNSYEKKIAVVASKVKGAVVRNRSKRILRALFAKFERYLQDGKY
IFVAKNEITELFSRLEKNLKWLKLECFK

Nucleotide sequence (minus strand):

AAGCAGCGGGTTTAAAGGGCTTAAGAATTCTGATAAAAACGGAGTATTTAGGCATATCATTGAAACATTCTA
GTTTTTCAATCCCATTAGATTCTAACCTAGAAAAAGAAAGTTCACTGATTCTATTAGCTACAAAA
ATATATTGCCATCTGAAGATATCTTCAAACTTAGCAAACAAAGCTCTAAATCGTTGAACGATTCTAAC
CACTGCTTCCAACTTTTACTAGCAACAACTGCTATTCTTCTACATAACTATTAGATAAAAAATGATCACAC
CTTCGCAATGCCATTTCGCTACTTATATACAGATGAAAATTCTCGTTGTGCTAAATTATCAAACATTTC
ACACAGCAAGTCTTTCTACCTTAGCGCGTCTGCATTGATCACTTGCGACCATTTTA

Sequence origin: Sanger centre & MDS

FIG. 2O

Vibrio cholerae serotype O1, Biotype El Tor, Strain N16961 (122 aa)

Amino acid sequence:

SRIILSTYAFNRELRLTPEHYQKVFQQAHSAGSPHLTIARANNLSPRLGLAVPKQIKTAVGRNRFKRICRESF
RLHQNLANKDFVVIAKSAQDLSNEELFNLLGKLWQRLSRPSRG

Nucleotide sequence (minus strand): *NO INITIATOR CODON BEFORE STOP*

GGCAGCGTGGCCGATAAGTGGACTAATAACCACCTGGTAAAGTTTACAATACCAATGGCTAACACGAGAAGGGC
GAGAGAGGCAGTGCATAGTTCCAAGCAAGTTAACAGTCTTCATTGCTCAAATCTGCGCCTCTTTGGCG
ATGACAACAAAATCTTGTAGCCAGTTGATGTAAGCGAAAGCTTCTCTGCAAATACGTTGAATCGATT
ACGGCCGACGGCAGTTGATCTGCTTTAGGAACCGCAGTCCAAACGAGGATGAGAAAGGTATTAGCGCAG
CGATGATTGTGAGATGAGGAGAACAGCACTGTGAGCTGCTGAAAGACTTTGATAATGTTGGGAGTTAACAAA
CGTAACCTCCGATTGAATGCGTACGTACTAAAATAATTGAGATTTTGACAGGCCTACGGCCTTGCACG
ACGTGCATTAGAACCTTACGACCCTCGC

Sequence origin: TIGR

FIG. 2G

Neisseria gonorrhoea FA 1090 (123 aa)

Amino acid sequence:

VILDYRFGRQYRLLKTDDFSSVFAFRNRRSRDLLQVSRSNGNLDHPRIGLVVGKKTAKRANERNYMKRVIRDWFRL
NKNRLPPQDFVVVRVRRKFDRATAKQARAELAQLMFGNPATGCGKQV

Nucleotide sequence (minus strand):

ATGTTCCCTGTATGGAAACCCGTTGCCGCTGAACCTGCCCTGCAGGGTACCGTTCTGATTCATACCTGTTCCCGC
ATCCGGTTGCGGGTTGCCGAAACATGAGTTGCCAGTTCCGCCCTGCCCTGTTTGCAGTAGCCCTGTCGAATTTC
CGGCAGCGCACGACGAAATCCTGAGGCCAGCCGGTTTGTCAATCTGAACCAGTCGCGGATGACGCGTT
CATATAGTTCCGCTGTTGCCGTTGGCGTTTTGCGACCACCGATGCCGGATGGTCCAGCCCGT
TGCCGTTGAGCGCAAACCTGCAGCGGCTGCCGGTTCTGAATGCAAAACGGATGAAAAATCATCC
GTTTTAACAAAGCGGTACTGCCCTCCGAAGCGGTAGTCAAATTACACTGCCAGGCCTTGCAGCCCTTGGCACGG
CGTGCAGGCCAATACTGCGCGTCCGCCCGT

Sequence origin: University of Oklahoma ACGT; Contig 60

FIG. 2H

Neisseria meningitidis serogroup A Strain Z2491 (123 aa)

Amino acid sequence:

VILDYRFGRQYRLLKTDDFSSVFAFRNRRSRDLLQVSRSNGNLDHPRIGLVVGKKTAKRANERNYMKRVIRDWFRL
NKNRLPPQDFVVVRVRRKFDRATAKQARAELAQLMFGNPATGCRKQA

Nucleotide sequence (minus strand):

TGTTCCCTAGTATGGAAACCCGTTGCCGCTGAACCTGCCCTGCAGAGTACCGTTCTGATTCATGCCTGTTCCCTGC
ATCCGGTTGCGGGTTGCCGAAACATGAGTTGCCAGTTCCGCCCTGCCCTGTTTGCAGTAGCCCTGTCGAATTTC
CGGCAGCGCACGACGAAATCCTGAGGCCAGCCGGTTTGTCAATCTGAACCAGTCGCGGATGACGCGTT
CATATAATTCTGTTGCCGTTGGCGGTTTGCAGGCCACCGACCGATGCCGGATGATCCAGCCCGT
TGCCGTTGAACCGCAAACCTGCAGCGGCTGCCGGTTCTGAATGCAAAACGGATGAAAAATCATCC
GTTTCAACAAAGCGGTACTGCCCTCCGAAGCGGTAGTCAAATTACACCGCCAGGCCTTGCAGCCCTTGGCGC
CGTGCAGGCCAATACTGCGCGTCCGCCCGC

Sequence origin: Sanger centre & Oxford University

FIG. 2I

Bacillus anthracis Ames (119 aa)

Amino acid sequence:

MKKKHKRIKKNDEFQTVFQKGKSANRQFVYQLDKEEQPNSKIGLVSKKIGNAVRNRIKRMIRQSITELKDEIDS
GKDFVIIARKPCAEMTYEELKSLIHVFKRSGMKRIKSSVRK

Nucleotide sequence (minus strand):

TAAACCTAATTCTTTCAAAGCCTACTCCTCCTGTATCGGTATGTATAAGTGTATTCATTCCCTACGGCTAC
TTTTTATTCTTTCATACCAGAGCGTTAAAGACATGAATTAAGCTTTCTTAATTCTCATATGTCATCTGCA
CAAGGCTCCTGCTATTATAACAAAATCTTCCAGAATCTATCTCATCTTAATTCTGTGATCGACTGGCGAAT
CATACGTTAATTGGTTACGCACTACTGCATTCTATCTTGTGACAGAAAGGCCAATACGAAAGTTGGCT
GCTCTTCTTATCTAGTTGATAGACAACAAATTGACGATTGCAATTGATTTCCTTTGAAAAACGTCTGGAAT
TCATCATTCTTTTATACGATTTTCTTCATATCAATTGACACTCCTGTAGTTCATCAGCGAAATTCACTAT
TATTAGAAAAAAAGACCA

Sequence origin: TIGR;

FIG. 2P

0 9 8 7 6 5 4 3 2 1 0

Mycobacterium avium 104 (119 aa)

Amino acid sequence:

VLPARNRMTRSTEFDATVKHGTRMAQPDIVHLRRDSEPDDESAGPRVGLVVGKAVGTAVQRHRVARRLRHVARALL
GELEPSDRLVIRALPGSRTASSARLAQELQRCLRRMPAGTGP

Nucleotide sequence (minus strand):

GTC CGC GGG CGACGGT CCG CC GG CG CA AT GG CG CG CC GAC CG CC GG GT CC GG T CACGGCCCGGT TCCC CG
CCGG CAT GC CG CG CAGG C ACC G CTG CAG TT CTG CG CC CAGG CG CG AC G AC G CG GT CC GG CT TCC CG GG CAG CG CG
CG AAT C ACC AG C CG GG T CGG AT GG TT CG AG T TC G CG C AG C AG GG CC GG CC AC GT G AC CG C AG CG CG GGG CC AC G CG
GT G CG TT G C ACC G CG GT CCC G AC GG C CT TCC G AC G ACC AG CC CG ACC CG TGG G CC CG GG ATT CG T CG T CGG GT
CG GAG T CG CG CC GG AG GT GG AC G AC G AT GT CG GG CT G CG CC AT G CG GT CC CG T CT ACC GT CG CG T CAA ACT CG
GT T G ACC G CG GT CAT G CG GT G CG T G CG GG AAG CAC CG CAA AG AC CT G AC GT G CG AT CAG G CAG AG AG CG CG CG
AC C TT G CG CG CG ACC

Sequence origin: TIGR;

FIG. 2Q

Staphylococcus aureus NCTC 8325 (117 aa)

Amino acid sequence:

MLLEKAYRIKKNADFQRIYKKGHSVANRQFVVYTCNNKEIDHFRLGISVSKLGNALRNKIKRAIRENFVKVHKSHI
LAKDIIVIARQPAKDMTTLQIQNSLEHVLKIAKVFNKIK

Nucleotide sequence (plus strand):

GTTATAAGCTCAATAGAAGTTAAATATAGCTCAAATAAAAACGATAAAATAAGCGAGTGATGTTATTGGAAAAGC
TTACCGAATTAAAAAGAATGCAGATTTCAGAGAATATATAAAAAGGTCAATTCTGTAGCCAACAGACAATTGTTG
TATACACTTGTAAATAATAAGAAATAGACCATTTCGCTTAGGTATTAGTGTCTAAAAAACTAGGTAATGCAGTG
TTAAGAAACAAGATTAAGAGCAATACGTGAAAATTCAAAGTACATAAGTCGCATATATTGGCAAAGATATTAT
TGTAAATAGCAAGACAGCCAGCTAAAGATATGACGACTTACAAATACAGAATAGTCTTGAGCACGTACTAAAATTG
CCAAAGTTTAATAAAAAGATTAAGTAAGGATAGGGTAGGGGAAGGAAACATTAACCACTCAACACATCCGAAG
TCTTACCTCAGA

Sequence origin: University of Oklahoma ACGT; Contig 561

FIG. 2R

Staphylococcus aureus COL (117 aa)

Amino acid sequence:

MLLEKAYRIKKNADFQRIYKKGHSVANRQFVVYTCNNKEIDHFRLGISVSKLGNALRNKIKRAIRENFVKVHKSHI
LAKDIIVIARQPAKDMTTLQIQNSLEHVLKIAKVFNKIK

Nucleotide sequence (plus strand):

GTTATAAGCTCAATAGAAGTTAAATATAGCTCAAATAAAAACGATAAAATAAGCGAGTGATGTTATTGGAAAAGC
TTACCGAATTAAAAAGAATGCAGATTTCAGAGAATATATAAAAAGGTCAATTCTGTAGCCAACAGACAATTGTTG
TATACACTTGTAAATAATAAGAAATAGACCATTTCGCTTAGGTATTAGTGTCTAAAAAACTAGGTAATGCAGTG
TTAAGAAACAAGATTAAGAGCAATACGTGAAAATTCAAAGTACATAAGTCGCATATATTGGCAAAGATATTAT
TGTAAATAGCAAGACAGCCAGCTAAAGATATGACGACTTACAAATACAGAATAGTCTTGAGCACGTACTAAAATTG
CCAAAGTTTAATAAAAAGATTAAGTAAGGATAGGGTAGGGGAAGGAAACATTAACCACTCAACACATCCGAAG
TCTTACCTCAGA

Sequence origin: TIGR;

FIG. 2S